Membrane Structure II

2063-Pos Board B200
Role of Headgroup Dipole Interactions in Phosphatidylcholine and Phosphatidylserine Bilayers
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The presence of a dielectric gradient in lipid bilayers is critical for membrane peptide folding in vivo. In addition, the hydrogen bonding ability of lipid head groups is known to affect bilayer properties. To reveal the role of headgroup dielectric properties in phospholipid bilayers, we have developed a polarizable Coarse-Grained (pCG) model, where the dipole moment of polar groups, such as serine and ester groups, can be adjusted through the addition of two extra "dummy" particles inside a CG bead. These dummy particles can mimic the hydrogen bonding network that can exist among head groups. The addition of polarization effects into CG beads has been proven effective in prior work regarding de novo peptide secondary structure folding with no external bias (Ganesan, 2014).
In this work, we have explored the role of dipole interactions in monocomponent lipid bilayers using POPC (Palmitoyl Oleoyl Phosphatidyl-Choline) and POPS (Palmitoyl Oleoyl Phosphatidyl-Serine) lipids. An excellent agreement is observed on several structural and dynamical bilayer properties when compared to all-atom simulation data.
We will present results on the role of dipole-dipole and dipole-charge interactions in shaping the clustering of PS lipids. Since dipole interactions are influenced by charge screening, the model is sensitive to changes in salt concentration. Our results suggest that headgroup dipole interactions may participate in PS/PC lipid phase separation as observed in experiments.
Reference
"The role of backbone dipole interactions in the formation of secondary and super-secondary structures of proteins", Ganesan S. J., Matysiak S., Journal of Chemical Theory and Computation (2014).

2064-Pos Board B201
Domain Formation in Quarternary Lipid Bilayer System: A Coarse-Grained Molecular Dynamics Study
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The spatial organization of phospholipids and sterols in cellular membranes is believed to play an important role in membrane function and cell activities. Both recent experimental and simulation studies have suggested various possible heterogeneous spatial distributions of lipids and cholesterol, including the formation of nanoscale lipid domains, in multi-component bilayer systems. In this study, we use coarse-grained Molecular Dynamics simulations to study the phase behavior of quarternary lipid mixtures as a function of membrane composition. We focus on the formation and size of nanoscopic lipid domains, their compositions, and their signatures in observables such as partial density correlation functions and structure factors.

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Investigating Lipid Phase Changes from Liquid Crystalline to Ripple to Gel Phases with All-Atom Molecular Dynamics Simulations
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Lipid mixed with water can exist in many different phases that depends on various factors, such as hydration, temperature and pressure (J. Chem. Theory Comput.,6 (8): 2488 (2010)). The liquid crystalline (chain-disordered state) is a well-studied phase for single lipid bilayers both experimentally and computationally. At low enough temperatures or hydration levels, this chain-disordered state can change to a gel state with high chain order and a certain chain tilt with respect to the membrane normal. Depending on the lipid, an intermediate phase can exist between the gel and liquid crystalline phase, which is known as the ripple phase. The main objective of this study was probing the accuracy of the CHARMM36 (C36) force field (FF) (J. Phys. Chem. B.,114 (23): 7830 (2010)) in predicting phase changes in lipid bilayers. Pure and mixed lipid bilayers at different compositions of 1,2-dimyristoyl-sn-glycero-3-phosphocholine (DMPC) and dipalmitoylphosphatidylcholine (DPPC) were studied using molecular dynamics (MD) simulations. Based on the pure gel-phase transition temperature of each lipid, a range of temperatures was selected (from 20^0C to 40^0C) (Biochem. 18: 3280 (1979)). MD simulations were able to capture ripple phase in %25 DMPC and %75 DPPC mixture and pure DMPC at 25^0C. Simulations were run for 200-300 ns. MD simulations also show either a gel state or gel-like state depending on if the system gets trapped (gel-like is a state without proper leaflet alignment). Phase diagram was compared to that obtained from experimental data such as NMR. Based on the phase diagram and our transition temperatures, C36 FF accurately predicts the phase transitions of this fully saturated PC lipids. Therefore, studies on phase coexistence of liquid ordered and liquid disordered domains are likely to be accurate using the C36 FF.

2066-Pos Board B203
Molecular Dynamics Simulations of Sphingomyelin-Cholesterol Bilayers
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Sphingolipids are one of the major components in animal cell membranes. One type of sphingolipids is sphingomyelins which are abundant in myelin sheath surrounding nerve cell axons. The two common forms of sphingomyelin targeted in this research are palmitoylsphingomyelin (PSM) and stearoylsphingomyelin (SSM). Another bilayer component included in our membranes that has high affinity to sphingomyelins is cholesterol, which aids in maintaining membrane fluidity and structural integrity. Sphingomyelins and cholesterol make up a great part of highly dynamic membrane domains, termed lipid rafts. With that being said, this work tests the accuracy of molecular dynamics (MD) simulations with the CHARMM36 (C36) lipid force field for PSM and SSM, each SM bilayer has varying concentrations of cholesterol. Properties such as surface area per lipid, x-ray and neutron form factors, and chain deuterium order parameters are to be compared to those yielded from past experiments to prove C36's ability to correctly simulate the mixed SM-cholesterol lipid bilayers. Based on past studies on C36 lipid force field, we expect to see excellent agreement between experimental and MD simulation data for more complex mixtures of membranes that contain SM lipids.

2067-Pos Board B204
Influence of Cholesterol on Phospholipid Bilayer Dynamics
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Surrounding every living cell is a membrane comprised of an assortment of lipids, cholesterol, and proteins. Bilayers are dynamic systems with phospholipid and cholesterol molecules diffusing within a leaflet and occasionally flipping between leaflets. In biological systems, bilayers can exist in two phases; liquid ordered or liquid disordered. Molecular dynamics (MD) simulations give windows of insight into the biophysical properties of these bilayers. In this study, the effects of cholesterol on lipid bilayers are investigated by examining a variety of phospholipid head groups, cholesterol concentrations, chain saturations, and chain lengths. Two fatty acid chains, dimyristoyl (DM) and dioleoyl (DO), were used in our initial simulations with a phosphatidylcholine head group. The DM chain was then studied with several other phospholipid head groups including phosphatidic acid, phosphatidylethanolamine, phosphatidylglycerol, phosphatidylinositol and phosphatidylserine. In order to ensure that the MD simulations are physically accurate, the systems were checked at different simulation sizes as well as compared to earlier simulations, X-ray diffraction experiments, and NMR data. Simulations between 50 and 150ns at temperatures of either 303.15 or 333.15K elucidated the lipid ordering and phase behavior of these lipids in liquid disordered and liquid ordered phases. Increases in cholesterol concentration were seen to increase order in liquid disordered bilayers while simultaneously promoting disorder in bilayers which form gels in pure bilayers at temperatures of 303.15K.

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Microscopic Model and Analytic Derivation of Area Per Molecule for DPPC-Cholesterol Bilayers
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An area per molecule dependence on components concentration for DPPC-Cholesterol bilayers is calculated analytically using a microscopic model in a biologically relevant concentration range. DPPC lipid is modeled as flexible string with finite bending rigidity [1,2]. Cholesterol molecule is modeled as rigid rod of finite thickness [3]. Surface tension at hydrophobic interface is linear combination of "partial tensions" of bilayer components. The model's three important parameters are: surface tension at hydrophobic interface for pure DPPC membrane, bending rigidity of DPPC lipid, extrapolated surface tension at hydrophobic interface for cholesterol membrane. These parameters are chosen by nearly perfect fitting agreement of our theoretical curve with molecular dynamics simulations data [4] for these two-component bilayers. The molecular